

0590
0906

OIKE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/939,293

DATE: 09/13/2001

TIME: 11:08:30

Input Set : A:\465.app.txt

Output Set: N:\CRF3\09132001\I939293.raw

4 <110> APPLICANT: Alnemri, Emad S.
 6 <120> TITLE OF INVENTION: AN IAP PEPTIDE OR POLYPEPTIDE
 7 AND METHODS OF USING THE SAME
 10 <130> FILE REFERENCE: 480140.465
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/939,293
 13 <141> CURRENT FILING DATE: 2001-08-24
 15 <160> NUMBER OF SEQ ID NOS: 18
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1358
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (20)...(739)
 28 <400> SEQUENCE: 1
 29 ggcgtccgcg cgctgcaca atg gcg gct ctg aag agt tgg ctg tcg cgc agc 52
 30 Met Ala Ala Leu Lys Ser Trp Leu Ser Arg Ser
 31 1 5 10
 33 gta act tca ttc ttc agg tac aga cag tgt ttg tgt gtt cct gtt gtg 100
 34 Val Thr Ser Phe Phe Arg Tyr Arg Gln Cys Leu Cys Val Pro Val Val
 35 15 20 25
 37 gct aac ttt aag aag cgg tgt ttc tca gaa ttg ata aga cca tgg cac 148
 38 Ala Asn Phe Lys Lys Arg Cys Phe Ser Glu Leu Ile Arg Pro Trp His
 39 30 35 40
 41 aaa act gtg acg att ggc ttt gga gta acc ctg tgt gcg gtt cct att 196
 42 Lys Thr Val Thr Ile Gly Phe Gly Val Thr Leu Cys Ala Val Pro Ile
 43 45 50 55 ~~56~~
 45 gca cag aaa tca gag cct cat tcc ctt agt agt gaa gca ttg atg agg 244
 46 Ala Gln Lys Ser Glu Pro His Ser Leu Ser Ser Glu Ala Leu Met Arg
 47 60 65 70 75
 49 aga gca gtg tct ttg gta aca gat agc acc tct acc ttt ctc tct cag 292
 50 Arg Ala Val Ser Leu Val Thr Asp Ser Thr Ser Thr Phe Leu Ser Gln
 51 80 85 90
 53 acc aca tat gcg ttg att gaa gct att act gaa tat act aag gct gtt 340
 54 Thr Thr Tyr Ala Leu Ile Glu Ala Ile Thr Glu Tyr Thr Lys Ala Val
 55 95 100 105
 57 tat acc tta act tct ctt tac cga caa tat aca agt tta ctt ggg aaa 388
 58 Tyr Thr Leu Thr Ser Leu Tyr Arg Gln Tyr Thr Ser Leu Leu Gly Lys
 59 110 115 120
 61 atg aat tca gag gag gaa gat gaa gtg tgg cag gtg atc ata gga gcc 436
 62 Met Asn Ser Glu Glu Glu Asp Glu Val Trp Gln Val Ile Ile Gly Ala
 63 125 130 135
 65 aga gct gag atg act tca aaa cac caa gag tac ttg aag ctg gaa acc 484
 66 Arg Ala Glu Met Thr Ser Lys His Gln Glu Tyr Leu Lys Leu Glu Thr
 67 140 145 150 155
 69 act tgg atg act gca gtt ggt ctt tca gag atg gca gca gaa gct gca 532

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70 Thr Trp Met Thr Ala Val Gly Leu Ser Glu Met Ala Ala Glu Ala Ala
71                               160                               165                               170
73 tat caa act ggc gca gat cag gcc tct ata acc gcc agg aat cac att      580
74 Tyr Gln Thr Gly Ala Asp Gln Ala Ser Ile Thr Ala Arg Asn His Ile
75                               175                               180                               185
77 cag ctg gtg aaa ctg cag gtg gaa gag gtg cac cag ctc tcc cgg aaa      628
78 Gln Leu Val Lys Leu Gln Val Glu Glu Val His Gln Leu Ser Arg Lys
79                               190                               195                               200
81 gca gaa acc aag ctg gca gaa gca cag ata gaa gag ctc cgt cag aaa      676
82 Ala Glu Thr Lys Leu Ala Glu Ala Gln Ile Glu Glu Leu Arg Gln Lys
83                               205                               210                               215
85 aca cag gag gaa ggg gag gag cgg gct gag tcg gag cag gag gcc tac      724
86 Thr Gln Glu Glu Gly Glu Glu Arg Ala Glu Ser Glu Gln Glu Ala Tyr
87 220                               225                               230                               235
89 ctg cgt gag gat tga gggcctgagc aactgcct gtctcccccac tcagtgggga      779
90 Leu Arg Glu Asp *
93 aagcaggggc agatgccacc ctgcccagggt ttggcatgac tgtctgtgca ccgagaagag      839
94 gcggcagggtc ctgcccctggc caatcaggcg agacgccttt gtgagctgtg agtgcctcct      899
95 gtggtctcag gcttgcgctg gacctggttc ttagcccttg ggcactgcac cctgtttaac      959
96 atttcacccc actctgtaca gctgctctta cccatttttt ttacctcaca cccaaagcat      1019
97 ttgcctacc tgggtcagag agaggagtc tttttgtcat gcccttaagt tcagcaactg      1079
98 tttaacctgt tttagctctt atttacgtcg tcaaaaatga ttagtactt gttccctctg      1139
99 ttgggatgcc agttgtggca gggggagggg aacctgtcca gtttgtacga tttctttgta      1199
100 tgtattttctg atgtgttctc tgatctgccc ccaactgtcct gtgaggacag ctgaggccaa      1259
101 ggagtgaata acctattact actaagagaa ggggtgcaga gtgtttacct ggtgctctca      1319
102 acaggactta acatcaacag gacttaacac agaaaaaaaaa                        1358
104 <210> SEQ ID NO: 2
105 <211> LENGTH: 40
106 <212> TYPE: PRT
107 <213> ORGANISM: Homo sapiens
109 <400> SEQUENCE: 2
110 Ala Val Pro Ile Ala Gln Lys Ser Glu Pro His Ser Leu Ser Ser Glu
111 1                               5                               10                               15
112 Ala Leu Met Arg Arg Ala Val Ser Leu Val Thr Asp Ser Thr Ser Thr
113                               20                               25                               30
114 Phe Leu Ser Gln Thr Thr Tyr Ala
115                               35                               40
118 <210> SEQ ID NO: 3
119 <211> LENGTH: 5
120 <212> TYPE: PRT
121 <213> ORGANISM: Homo sapiens
123 <220> FEATURE:
124 <221> NAME/KEY: VARIANT
125 <222> LOCATION: (4)...(4)
126 <223> OTHER INFORMATION: Xaa = Arg, Gln or Gly
128 <400> SEQUENCE: 3
W--> 129 Gln Ala Cys Xaa Gly
130 1                               5
133 <210> SEQ ID NO: 4

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134 <211> LENGTH: 7
135 <212> TYPE: PRT
136 <213> ORGANISM: Homo sapiens
138 <400> SEQUENCE: 4
139 Met Lys Ser Asp Phe Tyr Phe
140 1 5
143 <210> SEQ ID NO: 5
144 <211> LENGTH: 5
145 <212> TYPE: PRT
146 <213> ORGANISM: Homo sapiens
148 <400> SEQUENCE: 5
149 Ala Val Pro Ile Ala
150 1 5
153 <210> SEQ ID NO: 6
154 <211> LENGTH: 7
155 <212> TYPE: PRT
156 <213> ORGANISM: Homo sapiens
158 <400> SEQUENCE: 6
159 Ala Val Pro Ile Ala Gln Lys
160 1 5
163 <210> SEQ ID NO: 7
164 <211> LENGTH: 30
165 <212> TYPE: PRT
166 <213> ORGANISM: Homo sapiens
168 <400> SEQUENCE: 7
169 Ala Val Pro Ile Ala Gln Lys Ser Glu Pro His Ser Leu Ser Ser Glu
170 1 5 10 15
171 Ala Leu Met Arg Arg Ala Val Ser Leu Val Thr Asp Ser Thr
172 20 25 30
175 <210> SEQ ID NO: 8
176 <211> LENGTH: 39
177 <212> TYPE: PRT
178 <213> ORGANISM: Homo sapiens
180 <400> SEQUENCE: 8
181 Ala Val Pro Ile Ala Gln Lys Ser Glu Pro His Ser Leu Ser Ser Glu
182 1 5 10 15
183 Ala Leu Met Arg Arg Ala Val Ser Leu Val Thr Asp Ser Thr Ser Thr
184 20 25 30
185 Phe Leu Ser Gln Thr Thr Tyr
186 35
189 <210> SEQ ID NO: 9
190 <211> LENGTH: 9
191 <212> TYPE: PRT
192 <213> ORGANISM: Homo sapiens
194 <400> SEQUENCE: 9
195 Met Lys Ser Asp Phe Tyr Phe Gln Lys
196 1 5
199 <210> SEQ ID NO: 10
200 <211> LENGTH: 8

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```

201 <212> TYPE: PRT
202 <213> ORGANISM: Homo sapiens
204 <400> SEQUENCE: 10
205 Thr Asp Ser Thr Ser Thr Phe Leu
206 1 5
209 <210> SEQ ID NO: 11
210 <211> LENGTH: 35
211 <212> TYPE: PRT
212 <213> ORGANISM: Homo sapiens
214 <400> SEQUENCE: 11
215 Ala Val Pro Ile Ala Gln Lys Ser Glu Pro His Ser Leu Ser Ser Glu.
216 1 5 10 15
217 Ala Leu Met Arg Arg Ala Val Ser Leu Val Thr Asp Ser Thr Ser Thr
218 20 25 30
219 Phe Leu Ser
220 35
223 <210> SEQ ID NO: 12
224 <211> LENGTH: 9
225 <212> TYPE: PRT
226 <213> ORGANISM: Homo sapiens
228 <400> SEQUENCE: 12
229 Ile Glu Thr Asp Ala Val Pro Ile Ala
230 1 5
233 <210> SEQ ID NO: 13
234 <211> LENGTH: 4
235 <212> TYPE: PRT
236 <213> ORGANISM: Homo sapiens
238 <400> SEQUENCE: 13
239 Ala Val Pro Ile
240 1
243 <210> SEQ ID NO: 14
244 <211> LENGTH: 4
245 <212> TYPE: PRT
246 <213> ORGANISM: Homo sapiens
248 <400> SEQUENCE: 14
249 Ala Thr Pro Phe
250 1
253 <210> SEQ ID NO: 15
254 <211> LENGTH: 4
255 <212> TYPE: PRT
256 <213> ORGANISM: Drosophila sp.
258 <400> SEQUENCE: 15
259 Ala Val Ala Phe
260 1
263 <210> SEQ ID NO: 16
264 <211> LENGTH: 4
265 <212> TYPE: PRT
266 <213> ORGANISM: Drosophila sp.
268 <400> SEQUENCE: 16

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269 Ala Val Pro Phe
270 1
273 <210> SEQ ID NO: 17
274 <211> LENGTH: 4
275 <212> TYPE: PRT
276 <213> ORGANISM: Mus musculus
278 <400> SEQUENCE: 17
279 Ala Val Pro Tyr
280 1
283 <210> SEQ ID NO: 18
284 <211> LENGTH: 4
285 <212> TYPE: PRT
286 <213> ORGANISM: Xenopus sp.
288 <400> SEQUENCE: 18
289 Ala Thr Pro Val
290 1

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/939,293

DATE: 09/13/2001

TIME: 11:08:31

Input Set : A:\465.app.txt

Output Set: N:\CRF3\09132001\I939293.raw

L:12 M:270 C: Current Application Number differs, Wrong Format

L:129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3